

PATENT


IN THE UNITED STATES PATENT AND TRADEMARK OFFICE  
(Case No. 02-1270-A)


In application of	)	
	)	
J. Fruehauf, <i>et al.</i>	)	Examiner: Lei Yao
	)	
Serial No. 10/734,880	)	
	)	Group Art Unit: 1642
Filed: December 12, 2003	)	
	)	
For: Gene Related Sensitivity and Resistance	)	Confirmation No.: 1031
To Chemotherapeutic Drug Treatment	)	

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**APPENDIX B**





# Nucleotide

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Display  Show  Send to  Hide: ☐ sequence ☐ all but gene, CDS and mRNA features

Range: from  to 
☐ Reverse complemented strand
Features: ☐ SNP

1: [AF458589](#). Reports Homo sapiens myos...[gi:21360805]

[Links](#)

[Features](#) [Sequence](#)

LOCUS AF458589 4631 bp mRNA linear PRI 10-JUN-2002  
 DEFINITION Homo sapiens myosin phosphatase target subunit 1 variant (PPP1R12A) mRNA, complete cds.  
 ACCESSION AF458589  
 VERSION AF458589.1 GI:21360805  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 4631)  
 AUTHORS Guo, J.H., Chen, X.Y. and Yu, L.  
 TITLE Direct Submission  
 JOURNAL Submitted (15-DEC-2001) School of Life Sciences, Institute of Genetics, Fudan University, Handan Road, 220, Shanghai 200433, China

FEATURES

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## ORIGIN

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4621 tgtgaatttg t
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NCBI Nucleotide

PubMed Nucleotide Protein Genome Structure PMC Taxonomy OMM Books

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Display  Show  Send to Hide: ☐ sequence ☐ all but gene, CDS and mRNA features

Range: from  to  ☐ Reverse complemented strand Features:

☐ 1: [U79283](#). Reports Human albumin D-b...[gi:1710256]

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LOCUS HSU79283 1480 bp mRNA linear PRI 28-NOV-2000

DEFINITION Human albumin D-box binding protein mRNA, complete cds.

ACCESSION U79283

VERSION U79283.1 GI:1710256

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1480)

AUTHORS Andersson,B., Wentland,M.A., Ricafrente,J.Y., Liu,W. and Gibbs,R.A.

TITLE A 'double adaptor' method for improved shotgun library construction

JOURNAL Anal. Biochem. 236 (1), 107-113 (1996)

PUBMED 8619474

REFERENCE 2 (bases 1 to 1480)

AUTHORS Yu,W., Andersson,B., Worley,K.C., Muzny,D.M., Ding,Y., Liu,W., Ricafrente,J.Y., Wentland,M.A., Lennon,G. and Gibbs,R.A.

TITLE Large-scale concatenation cDNA sequencing

JOURNAL Genome Res. 7 (4), 353-358 (1997)

PUBMED 9110174

REFERENCE 3 (bases 1 to 1480)

AUTHORS Yu,W. and Gibbs,R.A.

TITLE Direct Submission

JOURNAL Submitted (22-NOV-1996) Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza S930, Houston, TX 77030, USA

FEATURES

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CDS




## ORIGIN

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Display  Show   Hide: ☐ sequence ☐ all but gene, CDS and mRNA features

Range: from  to  ☐ Reverse complemented strand Features: ☐ SNP ☒ MGC

☐ 1: [BC063851](#), Reports Homo sapiens comp...[gi:39645842]

Order cDNA clone,  
Links

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LOCUS BC063851 4015 bp mRNA linear PRI 15-JUL-2006  
 DEFINITION Homo sapiens complement component 7, mRNA (cDNA clone MGC:75123 IMAGE:6184213), complete cds.  
 ACCESSION BC063851  
 VERSION BC063851.1 GI:39645842  
 KEYWORDS MGC.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 4015)  
 REFERENCE  
 AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altshul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Schetz,T.E., Brownstein,M.J., Ustin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettelman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.  
 Mammalian Gene Collection Program Team  
 CONSRTM  
 TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences  
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  
 PUBMED [12477932](#)  
 REFERENCE 2 (bases 1 to 4015)  
 CONSRTM NIH MGC Project  
 TITLE Direct Submission  
 JOURNAL Submitted (08-DEC-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Bethesda, MD 20892-2590, USA  
 REMARK  
 COMMENT NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
 Contact: MGC help desk  
 Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
 Tissue Procurement: Dr. James R. Lupski  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Genome Sequence Centre,  
 BC Cancer Agency, Vancouver, BC, Canada  
[info@bcgsc.bc.ca](mailto:info@bcgsc.bc.ca)  
 Martin Hirst, Thomas Zeng, Ryan Morin, Michelle Moksa, Johnson Pang, Diana Mah, Jing Wang, Kieth Fichter, Eric Chuah, Allen Delaney, Rob Kirkpatrick, Agnes Baross, Sarah Barber, Mabel Brown-John, Steve S. Chand, William Chow, Ryan Babakaiff, Dave

Wong, Corey Matsuo, Jaclyn Beland, Susan Gibson, Luis delRio, Ruth Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao, Kim MacDonald, Mike R. Mayo, Josh Moran, Diana Palmquist, JR Santos, Duane Smailus, Jeff Stott, Miranda Tsai, George Yang, Jacquie Schein, Asim Siddiqui, Steven Jones, Rob Holt, Marco Marra.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
 Series: IRAK Plate: 141 Row: d Column: 14  
 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 45580687.

Differences found between this sequence and the human reference genome (build 36) are described in misc\_difference features below.

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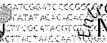


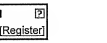
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Last update: Mon, 12 Jan 2009 Rev. 149544

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Range: from  to  ☐ Reverse complemented strand Features: ☐ SNP ☒ MGC

☐ 1: BC002788. Reports Homo sapiens plas...[gi:33877182]

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Comment Features Sequence

**LOCUS** BC002788 1353 bp mRNA linear PRI 15-JUL-2006  
**DEFINITION** Homo sapiens plasminogen activator, urokinase receptor, mRNA (cDNA clone MGC:3905 IMAGE:3617894), complete cds.  
**ACCESSION** BC002788  
**VERSION** BC002788.2 GI:33877182  
**KEYWORDS** MGC.  
**SOURCE** Homo sapiens (human)  
**ORGANISM** Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo.  
**REFERENCE** 1 (bases 1 to 1353)  
**AUTHORS** Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Schetz, T.E., Brownstein, M.J., Ustin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodrigues, Y., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.  
**CONSTRM** Mammalian Gene Collection Program Team  
**TITLE** Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences  
**JOURNAL** Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  
**PUBMED** 12477932  
**REFERENCE** 2 (bases 1 to 1353)  
**CONSTRM** NIH MGC Project  
**TITLE** Direct Submission  
**JOURNAL** Submitted (05-FEB-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Bethesda, MD 20892-2590, USA  
**REMARK** NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
**COMMENT** On Aug 19, 2003 this sequence version replaced gi:12803884.  
 Contact: MGC help desk  
 Email: cgapbs-r@mail.nih.gov  
 Tissue Procurement: ATCC/DCTD/DTF  
 cDNA Library Preparation: Rubin Laboratory  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),  
 Gaithersburg, Maryland;  
 Web site: <http://www.nisc.nih.gov/>  
 Contact: nisc\_mgc@nhgri.nih.gov  
 Akhtar, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,

Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R., Maduro, Q.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W., Turgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
 Series: IRAL Plate: 12 Row: j Column: 13  
 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 53829377.

Differences found between this sequence and the human reference genome (build 36) are described in misc\_difference features below.

## FEATURES

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## Location/Qualifiers

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## ORIGIN

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Last update: Mon, 12 Jan 2009 Rev. 149544

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Range: from  to  ☐ Reverse complemented strand Features: ☐ SNP ☒ MGC

☒ 1: BC005235. Reports Homo sapiens nucl...[gi:13528872]

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Comment Features Sequence

LOCUS BC005235 1199 bp mRNA linear PRI 15-JUL-2006  
 DEFINITION Homo sapiens nuclear DNA-binding protein, mRNA (cDNA clone MGC:12261 IMAGE:3930648), complete cds.  
 ACCESSION BC005235  
 VERSION BC005235.1 GI:13528872  
 KEYWORDS MGC.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 1199)  
 AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, P., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Ussin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.  
 Mammalian Gene Collection Program Team  
 CONSRTM TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences  
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  
 PUBMED 12477932  
 REFERENCE 2 (bases 1 to 1199)  
 CONSRTM NIH MGC Project  
 TITLE Direct Submission  
 JOURNAL Submitted (27-MAR-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Bethesda, MD 20892-2590, USA  
 REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
 COMMENT Contact: MGC help desk  
 Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
 Tissue Procurement: ATCC  
 cDNA Library Preparation: CLONTECH Laboratories, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305  
 Web site: <http://www-shgc.stanford.edu>  
 Contact: (Dickson, Mark) [mcd@paxil.stanford.edu](mailto:mcd@paxil.stanford.edu)  
 Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
 Series: IRAL Plate: 16 Row: 1 Column: 7  
 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 27894372.

Differences found between this sequence and the human reference genome (build 36) are described in misc difference features below and these differences were also compared to chimpanzee genome (build 2).

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ORIGIN


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Range: from
to
☐ Reverse complemented strand
Features:
☐ SNP

1: [AF060181](#). Reports Homo sapiens zinc...[gi:3228539]

[Links](#)

[Features](#) [Sequence](#)

LOCUS AF060181 4440 bp mRNA linear PRI 16-JUN-1998  
 DEFINITION Homo sapiens zinc finger protein (ZNF198) mRNA, complete cds.  
 ACCESSION AF060181  
 VERSION AF060181.1 GI:3228539  
 KEYWORDS .  
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 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;  
 Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 4440)  
 AUTHORS Still, I.H. and Cowell, J.K.  
 TITLE The t(8;13) atypical myeloproliferative disorder: further analysis  
 of the ZNF198 gene and lack of evidence for multiple genes  
 disrupted on chromosome 13  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 4440)  
 AUTHORS Still, I.H.  
 TITLE Direct Submission  
 JOURNAL Submitted (16-APR-1998) Neurosciences, Cleveland Clinic Foundation,  
 9500 Euclid Avenue, Cleveland, OH 44195, USA  
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## ORIGIN

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1: [AF237631](#). Reports Homo sapiens ubiq...[gi:7288860]

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LOCUS AF237631 2072 bp mRNA linear PRI 23-MAR-2000

DEFINITION Homo sapiens ubiquitous tropomodulin U-Tmod mRNA, complete cds.

ACCESSION AF237631

VERSION AF237631.1 GI:7288860

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
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 Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;  
 Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 2072)  
 AUTHORS Conley,C.A., Almenar-Queralta,A. and Fowler,V.M.  
 TITLE Identifying novel tropomodulin isoforms  
 JOURNAL Mol. Biol. Cell 9, 18A (1998)

REFERENCE 2 (bases 1 to 2072)  
 AUTHORS Conley,C.A. and Fowler,V.M.  
 TITLE Direct Submission  
 JOURNAL Submitted (23-FEB-2000) Space Life Sciences, NASA Ames Research  
 Center, M/S 239-11, Moffett Field, CA 94035-1000, USA

FEATURES

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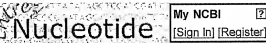
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Range: from  to  ☐ Reverse complemented strand Features: ☐ SNP

**1: D00099.** Reports Homo sapiens mRNA...[gi:219941]

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LOCUS HUMNKATPA 4108 bp mRNA linear PRI 11-MAR-1998  
 DEFINITION Homo sapiens mRNA for Na,K-ATPase alpha-subunit, complete cds.  
 ACCESSION D00099  
 VERSION D00099.1 GI:219941  
 KEYWORDS Na,K-ATPase; alpha-subunit.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;  
 Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 4108)  
 REFERENCE Kawakami,K., Ohta,T., Nojima,H. and Nagano,K.  
 TITLE Primary structure of the alpha-subunit of human Na,K-ATPase deduced  
 from cDNA sequence  
 JOURNAL J. Biochem. 100 (2), 389-397 (1986)  
 PUBMED 2430951  
 COMMENT The alpha-subunit of the human Na,K-ATPase exhibited 87% homology  
 with its Torpedo counterpart and 98% homology with its sheep  
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Last update: Mon, 12 Jan 2009 Rev. 149544



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LOCUS       BC002795                     2409 bp    mRNA    linear    PRI 19-MAR-2007
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ACCESSION   BC002795
VERSION     BC002795.2  GI:33877195
KEYWORDS    MGC.
SOURCE      Homo sapiens (human)
            ORGANISM      Homo sapiens

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## REFERENCE AUTHORS

Klausner, R.D., Collins, F.S., Wagner, L., Shennen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Ustin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalish, D.E., Schnierch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

CONSTRM Mammalian Gene Collection Program Team  
TITLE Generation and initial analysis of more than 15,000 full-length  
human and mouse cDNA sequences

JOURNAL  
PUBMED

REFERENCE 2 (bases 1 to 2409)

CONSRTM    NIH MGC Project

TITLE Direct Submission

JOURNAL Submitted (05-FEB-2001) National Institutes of Health, Mammalian  
Gene Collection (MGC), Bethesda, MD 20892-2590, USA

REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>

COMMENT On Aug 19, 2003 this sequence version replaced gi:12803896.

Contact: MGC help desk

Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)

Tissue Procurement: ATCC/DCTD/DTP

cDNA Library Preparation: Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC).

Gaithersburg, Maryland;

Web site: <http://www.nisc.nih.gov/>

Contact: nisc mgc@nhgri.nih.gov

Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,



Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R., Maduro, Q.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
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Differences found between this sequence and the human reference genome (build 36) are described in misc\_difference features below.

## FEATURES

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